

SEQUENCE LISTING

<110> Cahoon, Edgar B.
Cahoon, Rebecca E.
Kinney, Anthony J.
Rafalski, J. Antoni

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<151> 1988-04-30

<150> PCT/US99/09280

<151> 1999-04-29

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<151> 2000-10-30

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His Phe Ala Gln Thr Val Arg Asp Gly Val Leu Thr Lys Tyr Asp Tyr
          35           40           45
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Val Leu Pro Glu Arg Asn Ile Ala Ser Tyr Gly Gln Ala Glu Pro Pro
50 55 60

Val Tyr Arg Met Ser Gly Ile Pro Pro Ser Phe Pro Leu Phe Leu Ser
65 70 75 80

Tyr Gly Gly Arg Asp Ser Leu Ala Asp Pro Ala Asp Val Arg Leu Leu
85 90 95

Leu Gln Asp Leu Arg Gly His Asp Gln Asp Lys Leu Thr Val Gln Tyr
100 105 110

Leu Asp Lys Phe Ala His Leu Asp Phe Ile Ile Gly Val Cys Ala Lys
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Glu Ser Arg Pro Pro Val Tyr Asp Leu Ser Lys Ile Pro Leu Asp Ile
35 40 45

Pro Leu Phe Leu Ser Tyr Gly Gly Gln Asp Ala Leu Ser Asp Val Lys
50 55 60

Asp Val Glu Thr Leu Leu Asp Ser Leu Lys Leu His Asp Val Asp Lys
65 70 75 80

Leu His Val Gln Tyr Ile Lys Asp Tyr Ala His Ala Asp Phe Ile Ile
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Phe Leu Pro Gln Asn Asp Val Val Leu Pro Pro Asp Gly Val Cys Ser
35 40 45
Thr Ala Val Thr Val His Gly Tyr Lys Cys Gln Glu Phe Glu Val Thr
50 55 60
Thr Asp Asp Gly Tyr Ile Leu Ser Val Gln Arg Ile Leu Glu Gly Arg
65 70 75 80
Ala Gly Gly Gly Gly Gly Pro Lys Arg Pro Pro Val Leu Leu Gln His Gly
85 90 95
Val Leu Val Asp Gly Met Thr Trp Leu Val Asn Gly Pro Glu Gln Ser
100 105 110
Leu Ala Met Ile Leu Ala Asp Asn Gly Phe Asp Val Trp Ile Ser Asn
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 Pro Arg Ile Pro Ala His Arg Arg Ala Thr Pro Arg Leu Pro Ala Arg
 35 40 45
 Gly Gly Arg Trp Pro Leu Pro Ala Ala Ala Pro Ala Ala Gly Tyr Pro
 50 55 60
 Cys Thr Glu His Thr Val Gln Thr Asp Asp Gly Phe Leu Leu Ser Leu
 65 70 75 80
 Gln His Ile Pro His Gly Arg Asn Gly Ile Ala Asp Asn Thr Gly Pro
 85 90 95
 Pro Val Phe Leu Gln His Gly Leu Phe Gln Gly Gly Asp Thr Trp Phe
 100 105 110
 Ile Asn Ser Asn Glu Gln Ser Leu Gly Tyr Ile Leu Ala Asp Asn Gly
 115 120 125
 Phe Asp Val Trp Val Gly Asn Val Arg Gly Thr Arg Trp Ser Lys Gly
 130 135 140
 His Ser Thr Leu Ser Val His Asp Lys Leu Phe Trp Asp Trp Ser Trp
 145 150 155 160
 Gln Asp Leu Ala Glu Tyr Asp Val Leu Ala Met Leu Ser Tyr Val Tyr
 165 170 175
 Thr Val Ala Gln Ser Lys Ile Leu Tyr Val Gly His Ser Gln Gly Thr
 180 185 190
 Ile Met Gly Leu Ala Ala Phe Thr Met Pro Glu Thr Val Lys Met Ile
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 Ser Ser Ala Ala Leu Leu Cys Pro Ile Ser Tyr Leu Asp His Val Ser
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 Ala Ser Phe Val Leu Arg Ala Val Ala Met His Leu Asp Glu Met Leu
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 Arg Asn Thr Thr Asn Asp Ile Ser Asp Asp Lys Cys Pro Pro Gln Pro
 35 40 45
 His Pro Leu Xaa Met Cys Arg Ser Arg Val Ala Ala Tyr Gly Tyr Pro
 50 55 60

Cys Glu Glu Tyr His Val Thr Thr Glu Asp Gly Tyr Ile Leu Ser Leu
 65 70 75 80
 Lys Lys Ile Pro Tyr Gly Leu Ser Gly Xaa Thr Xaa Ile Thr Arg Xaa
 85 90 95
 Pro Val Leu Leu Phe His Gly Leu Leu Val Asp Gly Phe Cys Trp Val
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 35 40 45
 Val Ala Leu Ala Ala Phe Ser Glu Gly Arg Val Val Ser Gln Leu Lys
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      35             40             45

Gln Leu Leu Leu Pro Leu Gly Tyr Pro Cys Thr Glu His Asn Val Glu
      50             55             60

Thr Lys Asp Gly Phe Leu Leu Ser Leu Gln His Ile Pro His Gly Lys
      65             70             75             80

Asn Lys Ala Ala Asp Ser Thr Gly Pro Pro Val Phe Leu Gln His Gly
      85             90             95

Leu Phe Gln Gly Gly Asp Thr Trp Phe Ile Asn Ser Ala Glu Gln Ser
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Leu Gly Tyr Ile Leu Ala Asp Asn Gly Phe Asp Val Trp Ile Gly Asn
      115            120            125

Val Arg Gly Thr Arg Trp Ser Lys Gly His Ser Thr Phe Ser Val His
      130            135            140

Asp Lys Leu Phe Trp Asp Trp Ser Trp Gln Glu Leu Ala Glu Tyr Asp
      145            150            155            160

Leu Leu Ala Met Leu Gly Tyr Val Tyr Thr Val Thr Gln Ser Lys Ile
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Leu Tyr Val Gly His Ser Gln Gly Thr Ile Met Gly Leu Ala Ala Leu
      180            185            190

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Glu	Asn	Cys	Cys	Phe	Asn	Thr	Ser	Arg	Ile	Asp	Tyr	Tyr	Leu	Glu	Tyr
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Met	Ser	Val	Lys	Ala	Lys	Asp	Asp	Val	Tyr	Val	Asp	Leu	Ile	Arg	Phe
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 <222> (386)
 <223> n=A, C, G, or T

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 ggggtttctga ccaagtacga ctacgtgatg ccggacgcga acgtggccag gtacgggcag 180
 gncgaccgcg cggcgtagca catggcgggc atcccggcgt gggtcccat cttcctcagc 240
 tacggcggcc gggactcgct gtccnaccgc gccgatcgtc gccctcctcc tcgacgacn 300
 cngccncggc ggccacgtcg ggcaccggct catccgtgcc agtaacnttc nccatactcg 360
 cccacgnccn acttcgtcan tcgggnnttc tgcgc 395

<210> 16
 <211> 80
 <212> PRT
 <213> Oryza sativa

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 <222> (8)
 <223> Xaa=ANY AMINO ACID

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 <222> (10)..(11)
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 <222> (15)
 <223> Xaa=ANY AMINO ACID

<220>
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 <222> (61)
 <223> Xaa=ANY AMINO ACID

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 Ile Phe Leu Lys Tyr Glu Pro Gln Pro Thr Ser Thr Lys Thr Leu Ile
 20 25 30
 His Leu Ala Gln Thr Val Arg Asp Gly Val Leu Thr Lys Tyr Asp Tyr
 35 40 45
 Val Met Pro Asp Ala Asn Val Ala Arg Tyr Gly Gln Xaa Asp Pro Pro
 50 55 60
 Ala Tyr Asp Met Ala Ala Ile Pro Ala Trp Phe Pro Ile Phe Leu Ser
 65 70 75 80

<210> 17
 <211> 1718
 <212> DNA
 <213> Glycine max

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 cagcatctcc ctctcttcat tagctatggg ggaagagatg cactttcaga tgtccgtgat 1260
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<210> 18
 <211> 410
 <212> PRT
 <213> Glycine max

<400> 18
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 20 25 30
 Leu Gly Arg Asn Ile Asn Pro Ser Val Tyr Gly Ile Cys Ala Ser Ser
 35 40 45
 Val Ile Val His Gly Tyr Lys Cys Gln Glu His Glu Val Thr Thr Asp
 50 55 60
 Asp Gly Tyr Ile Leu Ser Leu Gln Arg Ile Pro Glu Gly Arg Gly Lys
 65 70 75 80
 Ser Ser Gly Ser Gly Thr Arg Lys Gln Pro Val Val Ile Gln His Gly
 85 90 95

Val	Leu	Val	Asp	Gly	Met	Thr	Trp	Leu	Leu	Asn	Pro	Pro	Glu	Gln	Asp		
			100					105					110				
Leu	Pro	Leu	Ile	Leu	Ala	Asp	Asn	Gly	Phe	Asp	Val	Trp	Ile	Ala	Asn		
		115					120					125					
Thr	Arg	Gly	Thr	Arg	Tyr	Ser	Arg	Arg	His	Ile	Ser	Leu	Asp	Pro	Ser		
	130					135					140						
Ser	Gln	Ala	Tyr	Trp	Asn	Trp	Ser	Trp	Asp	Glu	Leu	Val	Ser	Tyr	Asp		
145					150					155					160		
Phe	Pro	Ala	Val	Phe	Asn	Tyr	Val	Phe	Ser	Gln	Thr	Gly	Gln	Lys	Ile		
				165					170					175			
Asn	Tyr	Val	Gly	His	Ser	Leu	Gly	Thr	Leu	Val	Ala	Leu	Ala	Ser	Phe		
			180					185					190				
Ser	Glu	Gly	Lys	Leu	Val	Thr	Gln	Leu	Lys	Ser	Ala	Ala	Leu	Leu	Ser		
		195					200					205					
Pro	Ile	Ala	Tyr	Leu	Ser	His	Met	Asn	Thr	Ala	Leu	Gly	Val	Val	Ala		
	210					215					220						
Pro	Lys	Ser	Phe	Val	Gly	Glu	Ile	Thr	Thr	Leu	Phe	Gly	Leu	Ala	Glu		
225					230					235					240		
Phe	Asn	Pro	Lys	Gly	Leu	Ala	Val	Asp	Ala	Phe	Leu	Lys	Ser	Leu	Cys		
				245					250					255			
Ala	His	Pro	Gly	Ile	Asp	Cys	Tyr	Asp	Leu	Leu	Thr	Ala	Leu	Thr	Gly		
			260					265					270				
Lys	Asn	Cys	Cys	Leu	Asn	Ser	Ser	Thr	Val	Asp	Leu	Phe	Leu	Met	Asn		
	275						280					285					
Glu	Pro	Gln	Ser	Thr	Ser	Thr	Lys	Asn	Met	Val	His	Leu	Ala	Gln	Thr		
	290					295					300						
Val	Arg	Leu	Gly	Ala	Leu	Thr	Lys	Phe	Asn	Tyr	Val	Arg	Pro	Asp	Tyr		
305					310					315					320		
Asn	Ile	Met	His	Tyr	Gly	Glu	Ile	Phe	Pro	Pro	Ile	Tyr	Asn	Leu	Ser		
				325					330					335			
Asn	Ile	Pro	His	Asp	Leu	Pro	Leu	Phe	Ile	Ser	Tyr	Gly	Gly	Arg	Asp		
			340					345					350				
Ala	Leu	Ser	Asp	Val	Arg	Asp	Val	Glu	Asn	Leu	Leu	Asp	Lys	Leu	Lys		
		355					360					365					
Phe	His	Asp	Glu	Asn	Lys	Arg	Ser	Val	Gln	Phe	Ile	Gln	Glu	Tyr	Ala		
	370					375					380						
His	Ala	Asp	Tyr	Ile	Met	Gly	Phe	Asn	Ala	Lys	Asp	Leu	Val	Tyr	Asn		
385					390					395					400		
Ala	Val	Leu	Ser	Phe	Phe	Asn	His	Gln	Val								
				405				410									

<210> 19
 <211> 1438
 <212> DNA
 <213> Glycine max

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 caccaaaaaac agcaacacag tttgtgtgaa gagctcatta tcccctacgg ttacccttgc 180
 tccgagcata cgattcaaac gaaggatggt ttcttggttag gtcttcaacg tgtctcttct 240
 tcttcttctc ttcggcttcg gaaccatgga gatggaggcc ctccggttct gcttctgcat 300
 ggattattca tggcagggtga tgcattggtt ctaaatactc cggaacaatc acttggcttc 360
 atacttgcag atcatggttt tgatgtttgg gtaggaaacg tgcgtggaac acgctggagc 420
 catggacata tatctttatt agagaagaaa aagcaatttt gggattggag ttggcaggaa 480
 ttagccctgt atgatgttg cggaaatgatc aattacatta attcagtaac aaactcaaag 540
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 gagatagtag aaaagggttg ggctgcagct cttctatctc caatatcata cttggatcat 660
 gtcagtgcac ctcttgtag tagaatggtt aagatgcaca ttgatgagat gattcttacc 720
 atgggcattc atcaactaaa cttcaaaaagc gaatgggggg ccagtctctt ggtttcctta 780
 tgtgataccc gcctaagttg caatgacatg ctttcatcca taacagggaa gaattgttgc 840
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 aacttgaacc accttttcca gatgatccgc aaagggtacct actccaagta tgattatgga 960
 aagctaaaaa atctgataga gtacggcaag ttcaatccac caaagtctga tcttagtcgc 1020
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 atgattagtt ttttcaagtc atccggaaaa tttagtagta tgtaattgtt gcttccttcc 1260
 ggtatgatgg atgtaattac tgtaattggtc tacgggtcca tctattactg cacttactgt 1320
 aaagttgaaa tattaatatt ctgtggagtc caccttgatt ttctgtatgt atatatgatg 1380
 acagatatat aaagatcggc gtcgcgatgac ctgtttctgc aaaaaaaaaa aaaaaaaaaa 1438

<210> 20
 <211> 405
 <212> PRT
 <213> Glycine max

<400> 20
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 Leu Leu Gly Asn Gly Asn Pro Val Gln Cys Phe Asp Gly Gly Ser His
 20 25 30
 Gln Lys Gln Gln His Ser Leu Cys Glu Glu Leu Ile Ile Pro Tyr Gly
 35 40 45
 Tyr Pro Cys Ser Glu His Thr Ile Gln Thr Lys Asp Gly Phe Leu Leu
 50 55 60
 Gly Leu Gln Arg Val Ser Ser Ser Ser Ser Leu Arg Leu Arg Asn His
 65 70 75 80
 Gly Asp Gly Gly Pro Pro Val Leu Leu Leu His Gly Leu Phe Met Ala
 85 90 95
 Gly Asp Ala Trp Phe Leu Asn Thr Pro Glu Gln Ser Leu Gly Phe Ile
 100 105 110
 Leu Ala Asp His Gly Phe Asp Val Trp Val Gly Asn Val Arg Gly Thr
 115 120 125


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attattacct aggtgaatgg acataccacc acttcgctag agaggtttgg cttcatgaga 240
gcatagatgg aaatgtagtt accagaaacg agacggtatg tgatgattct ggtgaagacc 300
cgacctgtag caggtcggtc tatgggatga gcgtagcaga tcatcttgag tactatgatg 360
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tatacaacta cgttcgtgaa gttgatggat ccatacatcct gtcaagatac ccgcaagaac 480
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<210> 22
<211> 166
<212> PRT
<213> Zea mays

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<400> 22
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Val Glu Leu Met Thr Phe Gly Gln Pro Arg Ile Gly Asn Pro Ala Phe
          20             25             30

Ala Val Tyr Phe Gly Glu Gln Val Pro Arg Thr Ile Arg Val Thr His
          35             40             45

Gln Asn Asp Ile Val Pro His Leu Pro Pro Tyr Tyr Tyr Tyr Leu Gly
          50             55             60

Glu Trp Thr Tyr His His Phe Ala Arg Glu Val Trp Leu His Glu Ser
          65             70             75             80

Ile Asp Gly Asn Val Val Thr Arg Asn Glu Thr Val Cys Asp Asp Ser
          85             90             95

Gly Glu Asp Pro Thr Cys Ser Arg Ser Val Tyr Gly Met Ser Val Ala
          100            105            110

Asp His Leu Glu Tyr Tyr Asp Val Thr Leu His Ala Asp Ser Arg Gly
          115            120            125

Thr Cys Gln Phe Val Ile Gly Ala Ala Asn Gln Val Tyr Asn Tyr Val
          130            135            140

Arg Glu Val Asp Gly Ser Ile Ile Leu Ser Arg Tyr Pro Gln Glu Pro
          145            150            155            160

Gln Ala Leu Glu Ser Met
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<210> 23
<211> 1434
<212> DNA
<213> Zea mays

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<223> n=A, C, G, or T

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 atcatagtct gaattcgata attgttgcaa tcaggggaac tcaagagaac agtgtacaga 420
 attggataaa agacttgata tgggaagcagc ttgatctaag tnatccaaac atgccaaatg 480
 caaagggtgca cagtggattt ttctcctcgt ataacaatac aattttgctg ctatgctatca 540
 caagtgtctgt gcacaaggca agaaagtcac atggagatat caatgtcata gtgacaggcc 600
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 gtggcagtggt gcaactcatg acttttgggc agcctcgtgt tggcaatgct gcattcgct 720
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 gacgtctcca tcgttgaacc tagtgtaaca aacagattgg agcagttcta gataggcgga 1140
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 aaaatcatag gacgtttatg ctgattggna ggattgctnt ggtaatanat gancatgtaa 1380
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 <211> 296
 <212> PRT
 <213> Zea mays

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 <222> (50)
 <223> Xaa=ANY AMINO ACID

<220>
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 <222> (80)
 <223> Xaa=ANY AMINO ACID

<220>
 <221> UNSURE
 <222> (129)
 <223> Xaa=ANY AMINO ACID

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 Leu Ser Ala Ala Ser His Gly Arg Glu Leu Pro Val Lys Ser Ser Asp
 20 25 30
 Arg Ser Phe Ile Tyr Asn His Thr Leu Ala Lys Thr Leu Val Glu Tyr
 35 40 45
 Ala Xaa Ala Val Tyr Met Thr Asp Leu Thr Ala Leu Phe Thr Trp Thr
 50 55 60
 Cys Ser Arg Cys Asn Asp Leu Thr Gln Gly Phe Glu Met Arg Ser Xaa
 65 70 75 80
 Ile Val Asp Val Glu Lys Leu Leu Ala Gly Ile Val Gly Val Asp His
 85 90 95
 Ser Leu Asn Ser Ile Ile Val Ala Ile Arg Gly Thr Gln Glu Asn Ser
 100 105 110
 Val Gln Asn Trp Ile Lys Asp Leu Ile Trp Lys Gln Leu Asp Leu Ser
 115 120 125
 Xaa Pro Asn Met Pro Asn Ala Lys Val His Ser Gly Phe Phe Ser Ser
 130 135 140
 Tyr Asn Asn Thr Ile Leu Arg Leu Ala Ile Thr Ser Ala Val His Lys
 145 150 155 160
 Ala Arg Lys Ser Tyr Gly Asp Ile Asn Val Ile Val Thr Gly His Ser
 165 170 175
 Met Gly Gly Ala Met Ala Ser Phe Cys Ala Leu Asp Leu Ala Met Lys
 180 185 190
 Leu Gly Gly Gly Ser Val Gln Leu Met Thr Phe Gly Gln Pro Arg Val
 195 200 205
 Gly Asn Ala Ala Phe Ala Ser Tyr Phe Ala Lys Tyr Val Pro Asn Thr
 210 215 220
 Ile Arg Val Thr His Gly His Asp Ile Val Pro His Leu Pro Pro Tyr
 225 230 235 240

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Glu Leu Gly His Val His Val Gly Phe Leu Lys Ala Leu Gly Leu Gln
20 25 30
Glu Glu Asp Gly Lys Asp Ala Thr Arg Ala Phe Pro Xaa Gly Ala Pro
35 40 45
Asn Ala Val Pro Gly Lys Pro Leu Ala Tyr Tyr Ala Leu Arg Glu Glu
50 55 60
Val Gln Lys Gln Leu Gln Lys His Pro Asn Ala Asn Val Val Val Thr
65 70 75 80
Gly His Ser Leu Gly Ala Ala Leu Ala Thr Ile Phe Pro Ala Leu Leu
85 90 95
Ala Phe His Gly Glu Arg Gly Val Leu Asp Arg Leu Leu Ser Val Val
100 105 110
Thr Tyr Gly Gln Pro Arg Val Gly Asp Lys Val Phe Ala Gly Tyr Val
115 120 125
Arg Ala Asn Val Pro Val Glu Pro Leu Arg Val Val Tyr Arg Tyr Asp
130 135 140
Val Val Pro Arg Val Pro Phe Asp Ala Pro Pro Val Ala Asp Phe Ala
145 150 155 160
His Gly Gly Thr Cys Val Tyr Phe Asp Gly Trp Tyr Lys Gly Arg Glu
165 170 175
Ile Ala Lys Gly Gly Asp Ala Pro Asn Lys Asn Tyr Phe Asp Pro Arg
180 185 190
Tyr Leu Leu Ser Met Tyr Gly Asn Ala Trp Gly Asp Leu Phe Lys Gly
195 200 205
Ala Phe Leu Trp Ala Lys Glu Gly Lys Asp Tyr Arg Glu Gly Ala Val
210 215 220
Ser Leu Leu Tyr Arg Ala Thr Gly Leu Leu Val Pro Gly Ile Ala Ser
225 230 235 240
His Ser Pro Arg Asp Tyr Val Asn Ala Val Arg Leu Gly Ser Val Ala
245 250 255
Ser Ala

<210> 27
<211> 432
<212> DNA
<213> Oryza sativa
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<222> (7)
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 tttagcatcg ttcttggtgcc cttgacctct cttgttaagt atggatcgca ggaagttcaa 180
 ctcattgactt ttggacagcc tcgggtaggc aatccttctt ttgctgcgta cttcagtgac 240
 caagtcccga gaacaatccg tgtgacccat cagaatgaca ttgtcccaca cttgccacca 300
 tattttttgct accttggtgga atggacatat caccacttct cgagagaggt ttggcttcat 360
 gagaccatag taggaaatgt agttactagg aatgagacca tctgtgatgg atcaggcgag 420
 gaccaacat gc 432

<210> 28
 <211> 106
 <212> PRT
 <213> Oryza sativa

<400> 28
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 Gly Ser Gln Glu Val Gln Leu Met Thr Phe Gly Gln Pro Arg Val Gly
 20 25 30
 Asn Pro Ser Phe Ala Ala Tyr Phe Ser Asp Gln Val Pro Arg Thr Ile
 35 40 45
 Arg Val Thr His Gln Asn Asp Ile Val Pro His Leu Pro Pro Tyr Phe
 50 55 60
 Cys Tyr Leu Gly Glu Trp Thr Tyr His His Phe Ser Arg Glu Val Trp
 65 70 75 80
 Leu His Glu Thr Ile Val Gly Asn Val Val Thr Arg Asn Glu Thr Ile
 85 90 95
 Cys Asp Gly Ser Gly Glu Asp Pro Thr Cys
 100 105

<210> 29
 <211> 1234
 <212> DNA
 <213> Glycine max

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 ggtacgcatt cccggcattg gaaaaatgca tgggtggcttc atgaaagcct taggggtaca 240
 gaaaaatgtg ggggtggccta aggagattca aagggatgaa aatcttcccc cgttggccta 300
 ctatgttatt agggacattc taaggaaaagg tttgagttaa aatcctaata caaagtttat 360
 cattacgggt catagtttgg gtggagcact cgcaatcttg taccctacga tcatgttctt 420
 gcatgatgag aagttgctga ttgagaggtt ggaagggatc tacacgtttg ggcaaccaag 480
 agttggagat gaagcatatg cacagtatat gagacaaaaa ttgagggaaa attctatcag 540
 gtattgcagg tttgtttatt gcaatgacat agttccgagg ttgccctatg atgataagga 600
 cttgctcttc aagcactttg ggatctgcct tttctttaac aggcgctatg aactcaggat 660
 tctcgaagaa gagccgaata agaactattt ctgccatgg tgtgtgatac ccatgatgtt 720
 caatgctgtt ttggaactaa taaggagcct taccatagcg tacaaaaatg gacctcacta 780
 tagagaagga tggtttctct ttagtttcag gttggttggg ctgctgattc ctggcttacc 840
 tgctcacggg ccacaagatt atattaattc cactcttctg ggatcaattg aaaaacattt 900
 taaagcagat tgatgtgtcc gtatacatga tcattccata ccactacgta catgtgtatg 960
 gtcatgcaga ctaaaattta cataatcaag atttttagtt ttagaaaaaa tggtaataac 1020
 acttgattat gtatcatgtg aagaatagtt atgtatcata atgatcatga ataataaac 1080
 agtttgtcgt cagtacgagt tattgtatag taattaataa gctagggtta aagttgtttc 1140
 ctttggtgca tggattttatc attaatgaga tcaatgtgaa gtttgtttat ttcaaaaaaa 1200
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1234

<210> 30
 <211> 246
 <212> PRT
 <213> Glycine max

<400> 30
 His Leu Met Val Arg Ile Pro Gly Ile Gly Lys Met His Gly Gly Phe
 1 5 10 15
 Met Lys Ala Leu Gly Leu Gln Lys Asn Val Gly Trp Pro Lys Glu Ile
 20 25 30

<212> PRT
 <213> Glycine max

<400> 32
 His Glu Glu Arg Trp Pro Lys Glu Ile Glu Thr Asp Glu Asn Arg Pro
 1 5 10 15
 Arg Val Tyr Tyr Ser Ile Arg Asp Leu Leu Lys Lys Cys Leu Asn Arg
 20 25 30
 Asn Asp Lys Ala Lys Phe Ile Leu Thr Gly His Ser Leu Gly Gly Ala
 35 40 45
 Leu Ala Ile Leu Phe Pro Ala Met Leu Ile Leu His Ala Glu Thr Phe
 50 55 60
 Leu Leu Glu Arg Leu Glu Gly Val Tyr Thr Phe Gly Gln Pro Arg Val
 65 70 75 80
 Gly Asp Glu Thr Phe Ala Lys Tyr Met Glu Asn Gln Leu Lys His Tyr
 85 90 95
 Gly Ile Lys Tyr Phe Arg Phe Val Tyr Cys Asn Asp Ile Val Pro Arg
 100 105 110
 Leu Pro Phe Asp Glu Asp Ile Met Lys Phe Glu His Phe Gly Thr Cys
 115 120 125
 Leu Tyr Tyr Asp Arg Ser Tyr Thr Cys Lys Val His Ile
 130 135 140

<210> 33
 <211> 774
 <212> DNA
 <213> Triticum aestivum

<400> 33
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 gcaacctcgg attggtaatg ctgtgtttgc taccacttt aagaaatact tgccaaacgc 180
 aattcgagtt accaacgcac atgatattgt gcctcatcta cccccgtact accagtactt 240
 cccacagaat acctaccatc atttcccacc agaggtttgg gttcataaca ttggactcga 300
 tagcctacta taccggatcg agcacatctg tgatcattct ggagaaagac cccacttgca 360
 gcaggcccctt ggttggaat agcgtccagg cccatacccc ctttcttggc tccagcatcc 420
 atccccgagtc gcgcggatca tccagaatcg tcacggatga caatatgctc aggcacaaag 480
 ttgcccctgt agacgggtgt attgtcttct cgaagcagcc tggtttatca gttggtcagc 540
 tactcagtac acagtaaaca agctcaagat tacatggatt tattttgatg tttttttttg 600
 ccaaagaaca atattcttgt tggcaatcaa agcactatct catgtatata tacgcgtgtg 660
 atcctggctg gattaaatta tcctagctga ggggtgtatt ctgaaatgta caaacatatc 720
 tatgctgatt aaaaaaaaaa aaaaaaatac ttgaggcggc cccgtaccaa aaat 774

<210> 34
 <211> 126
 <212> PRT
 <213> Triticum aestivum

<400> 34
 His Glu Asn Ile Pro Ile Met Val Thr Gly His Ser Met Gly Gly Ala
 1 5 10 15

Met Ala Ser Phe Cys Ala Leu Asp Leu Ile Val Asn Tyr Gly Leu Lys
 20 25 30
 Asp Val Thr Leu Leu Thr Phe Gly Gln Pro Arg Ile Gly Asn Ala Val
 35 40 45
 Phe Ala Thr His Phe Lys Lys Tyr Leu Pro Asn Ala Ile Arg Val Thr
 50 55 60
 Asn Ala His Asp Ile Val Pro His Leu Pro Pro Tyr Tyr Gln Tyr Phe
 65 70 75 80
 Pro Gln Asn Thr Tyr His His Phe Pro Pro Glu Val Trp Val His Asn
 85 90 95
 Ile Gly Leu Asp Ser Leu Leu Tyr Pro Ile Glu His Ile Cys Asp His
 100 105 110
 Ser Gly Glu Arg Pro His Leu Gln Gln Ala Leu Gly Trp Lys
 115 120 125

 <210> 35
 <211> 398
 <212> PRT
 <213> Canis familiaris

 <400> 35
 Met Trp Leu Leu Leu Thr Ala Ala Ser Val Ile Ser Thr Leu Gly Thr
 1 5 10 15
 Thr His Gly Leu Phe Gly Lys Leu His Pro Thr Asn Pro Glu Val Thr
 20 25 30
 Met Asn Ile Ser Gln Met Ile Thr Tyr Trp Gly Tyr Pro Ala Glu Glu
 35 40 45
 Tyr Glu Val Val Thr Glu Asp Gly Tyr Ile Leu Gly Ile Asp Arg Ile
 50 55 60
 Pro Tyr Gly Arg Lys Asn Ser Glu Asn Ile Gly Arg Arg Pro Val Ala
 65 70 75 80
 Phe Leu Gln His Gly Leu Leu Ala Ser Ala Thr Asn Trp Ile Ser Asn
 85 90 95
 Leu Pro Asn Asn Ser Leu Ala Phe Ile Leu Ala Asp Ala Gly Tyr Asp
 100 105 110
 Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ala Arg Arg Asn Leu
 115 120 125
 Tyr Tyr Ser Pro Asp Ser Val Glu Phe Trp Ala Phe Ser Phe Asp Glu
 130 135 140
 Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asp Phe Ile Leu Lys Lys
 145 150 155 160
 Thr Gly Gln Asp Lys Leu His Tyr Val Gly His Ser Gln Gly Thr Thr
 165 170 175

Ile Gly Phe Ile Ala Phe Ser Thr Asn Pro Lys Leu Ala Lys Arg Ile
 180 185 190
 Lys Thr Phe Tyr Ala Leu Ala Pro Val Ala Thr Val Lys Tyr Thr Glu
 195 200 205
 Thr Leu Leu Asn Lys Leu Met Leu Val Pro Ser Phe Leu Phe Lys Leu
 210 215 220
 Ile Phe Gly Asn Lys Ile Phe Tyr Pro His His Phe Phe Asp Gln Phe
 225 230 235 240
 Leu Ala Thr Glu Val Cys Ser Arg Glu Thr Val Asp Leu Leu Cys Ser
 245 250 255
 Asn Ala Leu Phe Ile Ile Cys Gly Phe Asp Thr Met Asn Leu Asn Met
 260 265 270
 Ser Arg Leu Asp Val Tyr Leu Ser His Asn Pro Ala Gly Thr Ser Val
 275 280 285
 Gln Asn Val Leu His Trp Ser Gln Ala Val Lys Ser Gly Lys Phe Gln
 290 295 300
 Ala Phe Asp Trp Gly Ser Pro Val Gln Asn Met Met His Tyr His Gln
 305 310 315 320
 Ser Met Pro Pro Tyr Tyr Asn Leu Thr Asp Met His Val Pro Ile Ala
 325 330 335
 Val Trp Asn Gly Gly Asn Asp Leu Leu Ala Asp Pro His Asp Val Asp
 340 345 350
 Leu Leu Leu Ser Lys Leu Pro Asn Leu Ile Tyr His Arg Lys Ile Pro
 355 360 365
 Pro Tyr Asn His Leu Asp Phe Ile Trp Ala Met Asp Ala Pro Gln Ala
 370 375 380
 Val Tyr Asn Glu Ile Val Ser Met Met Gly Thr Asp Asn Lys
 385 390 395

<210> 36
 <211> 403
 <212> PRT
 <213> *Caenorhabditis elegans*

<400> 36
 Met Trp Arg Phe Ala Val Phe Leu Ala Ala Phe Phe Val Gln Asp Val
 1 5 10 15
 Val Gly Ser His Gly Asp Pro Glu Leu His Met Thr Thr Pro Gln Ile
 20 25 30
 Ile Glu Arg Trp Gly Tyr Pro Ala Met Ile Tyr Thr Val Ala Thr Asp
 35 40 45
 Asp Gly Tyr Ile Leu Glu Met His Arg Ile Pro Phe Gly Lys Thr Asn
 50 55 60

Val	Thr	Trp	Pro	Asn	Gly	Lys	Arg	Pro	Val	Val	Phe	Met	Gln	His	Gly	
65					70					75					80	
Leu	Leu	Cys	Ala	Ser	Ser	Asp	Trp	Val	Val	Asn	Leu	Pro	Asp	Gln	Ser	
				85					90					95		
Ala	Gly	Phe	Leu	Phe	Ala	Asp	Ala	Gly	Phe	Asp	Val	Trp	Leu	Gly	Asn	
			100					105					110			
Met	Arg	Gly	Asn	Thr	Tyr	Ser	Met	Lys	His	Lys	Asp	Leu	Lys	Pro	Ser	
		115					120					125				
His	Ser	Ala	Phe	Trp	Asp	Trp	Ser	Trp	Asp	Glu	Met	Ala	Thr	Tyr	Asp	
	130					135					140					
Leu	Asn	Ala	Met	Ile	Asn	His	Val	Leu	Glu	Val	Thr	Gly	Gln	Asp	Ser	
145					150					155					160	
Val	Tyr	Tyr	Met	Gly	His	Ser	Gln	Gly	Thr	Leu	Thr	Met	Phe	Ser	His	
				165					170					175		
Leu	Ser	Lys	Asp	Asp	Gly	Ser	Phe	Ala	Lys	Lys	Ile	Lys	Lys	Phe	Phe	
			180					185					190			
Ala	Leu	Ala	Pro	Ile	Gly	Ser	Val	Lys	His	Ile	Lys	Gly	Phe	Leu	Ser	
		195					200					205				
Phe	Phe	Ala	Asn	Tyr	Phe	Ser	Leu	Glu	Phe	Asp	Gly	Trp	Phe	Asp	Ile	
	210					215					220					
Phe	Gly	Ala	Gly	Glu	Phe	Leu	Pro	Asn	Asn	Trp	Ala	Met	Lys	Leu	Ala	
225					230					235					240	
Ala	Lys	Asp	Ile	Cys	Gly	Gly	Leu	Lys	Val	Glu	Ala	Asp	Leu	Cys	Asp	
				245					250					255		
Asn	Val	Leu	Phe	Leu	Ile	Ala	Gly	Pro	Glu	Ser	Asp	Gln	Trp	Asn	Gln	
			260					265						270		
Thr	Arg	Val	Pro	Val	Tyr	Ala	Thr	His	Asp	Pro	Ala	Gly	Thr	Ser	Thr	
		275					280					285				
Gln	Asn	Ile	Val	His	Trp	Met	Gln	Met	Val	His	His	Gly	Gly	Val	Pro	
	290					295					300					
Ala	Tyr	Asp	Trp	Gly	Thr	Lys	Thr	Asn	Lys	Lys	Lys	Tyr	Gly	Gln	Ala	
305					310					315					320	
Asn	Pro	Pro	Glu	Tyr	Asp	Phe	Thr	Ala	Ile	Lys	Gly	Thr	Lys	Ile	Tyr	
				325					330					335		
Leu	Tyr	Trp	Ser	Asp	Ala	Asp	Trp	Leu	Ala	Asp	Thr	Pro	Asp	Val	Pro	
			340					345					350			
Asp	Tyr	Leu	Leu	Thr	Arg	Leu	Asn	Pro	Ala	Ile	Val	Ala	Gln	Asn	Asn	
		355					360					365				
His	Leu	Pro	Asp	Tyr	Asn	His	Leu	Asp	Phe	Thr	Trp	Gly	Leu	Arg	Ala	
	370					375					380					

Pro Asp Asp Ile Tyr Arg Pro Ala Ile Lys Leu Cys Thr Asp Asp Tyr
385 390 395 400

Leu Gly Lys